



SEQUENCE LISTING

<110> Detmar, Michael J.
Streit, Michael

<120> THROMBOSPONDIN-2 AND USES THEREOF

<130> 10287-051002

<140> 09/822,682

<141> 2001-03-30

<150> 09/536,087

<151> 2000-03-24

<150> 60/127,221

<151> 1999-03-31

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3596

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)...(3541)

<400> 1

caggagctca gctgcaggag gcagg atg gtc tgg agg ctg gtc ctg ctg gct	52
Met Val Trp Arg Leu Val Leu Leu Ala	
1 5	
ctg tgg gtg tgg ccc agc acg caa gct ggt cac cag gac aaa gac acg	100
Leu Trp Val Trp Pro Ser Thr Gln Ala Gly His Gln Asp Lys Asp Thr	
10 15 20 25	
acc ttc gac ctt ttc agt atc agc aac atc aac cgc aag acc att ggc	148
Thr Phe Asp Leu Phe Ser Ile Ser Asn Ile Asn Arg Lys Thr Ile Gly	
30 35 40	
gcc aag cag ttc cgc ggg ccc gac ccc ggc gtg ccg gct tac cgc ttc	196
Ala Lys Gln Phe Arg Gly Pro Asp Pro Gly Val Pro Ala Tyr Arg Phe	
45 50 55	
gtg cgc ttt gac tac atc cca ccg gtg aac gca gat gac ctc agc aag	244
Val Arg Phe Asp Tyr Ile Pro Pro Val Asn Ala Asp Asp Leu Ser Lys	
60 65 70	
atc acc aag atc atg cgg cag aag gag ggc ttc ttc ctc acg gcc cag	292
Ile Thr Lys Ile Met Arg Gln Lys Glu Gly Phe Phe Leu Thr Ala Gln	
75 80 85	

ctc aag cag gac ggc aag tcc agg ggc acg ctg ttg gct ctg gag ggc Leu Lys Gln Asp Gly Lys Ser Arg Gly Thr Leu Leu Ala Leu Glu Gly 90 95 100 105	340
ccc ggt ctc tcc cag agg cag ttc gag atc gtc tcc aat ggc ccc gcg Pro Gly Leu Ser Gln Arg Gln Phe Glu Ile Val Ser Asn Gly Pro Ala 110 115 120	388
gac acg ctg gat ctc acc tac tgg att gac ggc acc cgg cat gtg gtc Asp Thr Leu Asp Leu Thr Tyr Trp Ile Asp Gly Thr Arg His Val Val 125 130 135	436
tcc ctg gag gac gtc ggc ctg gct gac tcg cag tgg aag aac gtc acc Ser Leu Glu Asp Val Gly Leu Ala Asp Ser Gln Trp Lys Asn Val Thr 140 145 150	484
gtg cag gtg gct ggc gag acc tac agc ttg cac gtg ggc tgc gac ctc Val Gln Val Ala Gly Glu Thr Tyr Ser Leu His Val Gly Cys Asp Leu 155 160 165	532
ata gac agc ttc gct ctg gac gag ccc ttc tac gag cac ctg cag gcg Ile Asp Ser Phe Ala Leu Asp Glu Pro Phe Tyr Glu His Leu Gln Ala 170 175 180 185	580
gaa aag agc cgg atg tac gtg gcc aaa ggc tct gcc aga gag agt cac Glu Lys Ser Arg Met Tyr Val Ala Lys Gly Ser Ala Arg Glu Ser His 190 195 200	628
ttc agg ggt ttg ctt cag aac gtc cac cta gtg ttt gaa aac tct gtg Phe Arg Gly Leu Leu Gln Asn Val His Leu Val Phe Glu Asn Ser Val 205 210 215	676
gaa gat att cta agc aag aag ggt tgc cag caa ggc cag gga gct gag Glu Asp Ile Leu Ser Lys Lys Gly Cys Gln Gln Gly Gln Gly Ala Glu 220 225 230	724
atc aac gcc atc agt gag aac aca gag acg ctg cgc ctg ggt ccg cat Ile Asn Ala Ile Ser Glu Asn Thr Glu Thr Leu Arg Leu Gly Pro His 235 240 245	772
gtc acc acc gag tac gtg ggc ccc agc tca gag agg agg ccc gag gtg Val Thr Thr Glu Tyr Val Gly Pro Ser Ser Glu Arg Arg Pro Glu Val 250 255 260 265	820
tgc gaa cgc tcg tgc gag gag ctg gga aac atg gtc cag gag ctc tcg Cys Glu Arg Ser Cys Glu Glu Leu Gly Asn Met Val Gln Glu Leu Ser 270 275 280	868
ggg ctc cac gtc ctc gtg aac cag ccc agc gag aac ctc aag aga gtg Gly Leu His Val Leu Val Asn Gln Pro Ser Glu Asn Leu Lys Arg Val 285 290 295	916
tcg aat gat aac cag ttt ctc tgg gag ctc att ggt ggc cct cct aag Ser Asn Asp Asn Gln Phe Leu Trp Glu Leu Ile Gly Gly Pro Pro Lys 300 305 310	964
aca agg aac atg tca gct tgc tgg cag gat ggc cgg ttc ttt gcg gaa	1012

Thr	Arg	Asn	Met	Ser	Ala	Cys	Trp	Gln	Asp	Gly	Arg	Phe	Phe	Ala	Glu		
	315					320					325						
aat	gaa	acg	tgg	gtg	gtg	gac	agc	tgc	acc	acg	tgt	acc	tgc	aag	aaa	1060	
Asn	Glu	Thr	Trp	Val	Val	Asp	Ser	Cys	Thr	Thr	Cys	Thr	Cys	Lys	Lys		
330					335					340					345		
ttt	aaa	acc	att	tgc	cac	caa	atc	acc	tgc	ccg	cct	gca	acc	tgc	gcc	1108	
Phe	Lys	Thr	Ile	Cys	His	Gln	Ile	Thr	Cys	Pro	Pro	Ala	Thr	Cys	Ala		
				350					355						360		
agt	cca	tcc	ttt	gtg	gaa	ggc	gaa	tgc	tgc	cct	tcc	tgc	ctc	cac	tcg	1156	
Ser	Pro	Ser	Phe	Val	Glu	Gly	Glu	Cys	Cys	Pro	Ser	Cys	Leu	His	Ser		
			365					370					375				
gtg	gac	ggg	gag	gag	ggc	tgg	tct	ccg	tgg	gca	gag	tgg	acc	cag	tgc	1204	
Val	Asp	Gly	Glu	Glu	Gly	Trp	Ser	Pro	Trp	Ala	Glu	Trp	Thr	Gln	Cys		
		380					385					390					
tcc	gtg	acg	tgt	ggc	tct	ggg	acc	cag	cag	aga	ggc	cgg	tcc	tgt	gac	1252	
Ser	Val	Thr	Cys	Gly	Ser	Gly	Thr	Gln	Gln	Arg	Gly	Arg	Ser	Cys	Asp		
	395					400					405						
gtc	acc	agc	aac	acc	tgc	ttg	ggg	ccc	tcc	atc	cag	aca	cgg	gct	tgc	1300	
Val	Thr	Ser	Asn	Thr	Cys	Leu	Gly	Pro	Ser	Ile	Gln	Thr	Arg	Ala	Cys		
410					415				420						425		
agt	ctg	agc	aag	tgt	gac	acc	cgc	atc	cgg	cag	gac	ggc	ggc	tgg	agc	1348	
Ser	Leu	Ser	Lys	Cys	Asp	Thr	Arg	Ile	Arg	Gln	Asp	Gly	Gly	Trp	Ser		
				430					435					440			
cac	tgg	tca	cct	tgg	tct	tca	tgc	tct	gtg	acc	tgt	gga	ggt	ggc	aat	1396	
His	Trp	Ser	Pro	Trp	Ser	Ser	Cys	Ser	Val	Thr	Cys	Gly	Val	Gly	Asn		
			445					450					455				
atc	aca	cgc	atc	cgt	ctc	tgc	aac	tcc	cca	gtg	ccc	cag	atg	ggg	ggc	1444	
Ile	Thr	Arg	Ile	Arg	Leu	Cys	Asn	Ser	Pro	Val	Pro	Gln	Met	Gly	Gly		
		460					465					470					
aag	aat	tgc	aaa	ggg	agt	ggc	cgg	gag	acc	aaa	gcc	tgc	cag	ggc	gcc	1492	
Lys	Asn	Cys	Lys	Gly	Ser	Gly	Arg	Glu	Thr	Lys	Ala	Cys	Gln	Gly	Ala		
	475					480					485						
cca	tgc	cca	atc	gat	ggc	cgc	tgg	agc	ccc	tgg	tcc	ccg	tgg	tcg	gcc	1540	
Pro	Cys	Pro	Ile	Asp	Gly	Arg	Trp	Ser	Pro	Trp	Ser	Pro	Trp	Ser	Ala		
490					495					500					505		
tgc	act	gtc	acc	tgt	gcc	ggg	ggg	atc	cgg	gag	cgc	acc	cgg	gtc	tgc	1588	
Cys	Thr	Val	Thr	Cys	Ala	Gly	Gly	Ile	Arg	Glu	Arg	Thr	Arg	Val	Cys		
				510					515					520			
aac	agc	cct	gag	cct	cag	tac	gga	ggg	aag	gcc	tgc	gtg	ggg	gat	gtg	1636	
Asn	Ser	Pro	Glu	Pro	Gln	Tyr	Gly	Gly	Lys	Ala	Cys	Val	Gly	Asp	Val		
			525					530					535				
cag	gag	cgt	cag	atg	tgc	aac	aag	agg	agc	tgc	ccc	gtg	gat	ggc	tgt	1684	
Gln	Glu	Arg	Gln	Met	Cys	Asn	Lys	Arg	Ser	Cys	Pro	Val	Asp	Gly	Cys		

540	545	550	
tta tcc aac ccc tgc ttc ccg gga gcc cag tgc agc agc ttc ccc gat Leu Ser Asn Pro Cys Phe Pro Gly Ala Gln Cys Ser Ser Phe Pro Asp 555 560 565			1732
ggg tcc tgg tca tgc ggc tcc tgc cct gtg ggc ttc ttg ggc aat ggc Gly Ser Trp Ser Cys Gly Ser Cys Pro Val Gly Phe Leu Gly Asn Gly 570 575 580 585			1780
acc cac tgt gag gac ctg gac gag tgt gcc ctg gtc ccc gac atc tgc Thr His Cys Glu Asp Leu Asp Glu Cys Ala Leu Val Pro Asp Ile Cys 590 595 600			1828
ttc tcc acc agc aag gtg cct cgc tgt gtc aac act cag cct ggc ttc Phe Ser Thr Ser Lys Val Pro Arg Cys Val Asn Thr Gln Pro Gly Phe 605 610 615			1876
cac tgc ctg ccc tgc ccg ccc cga tac aga ggg aac cag ccc gtc ggg His Cys Leu Pro Cys Pro Pro Arg Tyr Arg Gly Asn Gln Pro Val Gly 620 625 630			1924
gtc ggc ctg gaa gca gcc aag acg gaa aag caa gtg tgt gag ccc gaa Val Gly Leu Glu Ala Ala Lys Thr Glu Lys Gln Val Cys Glu Pro Glu 635 640 645			1972
aac cca tgc aag gac aag aca cac aac tgc cac aag cac gcg gag tgc Asn Pro Cys Lys Asp Lys Thr His Asn Cys His Lys His Ala Glu Cys 650 655 660 665			2020
atc tac ctg ggc cac ttc agc gac ccc atg tac aag tgc gag tgc cag Ile Tyr Leu Gly His Phe Ser Asp Pro Met Tyr Lys Cys Glu Cys Gln 670 675 680			2068
aca ggc tac gcg ggc gac ggg ctc atc tgc ggg gag gac tcg gac ctg Thr Gly Tyr Ala Gly Asp Gly Leu Ile Cys Gly Glu Asp Ser Asp Leu 685 690 695			2116
gac ggc tgg ccc aac ctc aat ctg gtc tgc gcc acc aac gcc acc tac Asp Gly Trp Pro Asn Leu Asn Leu Val Cys Ala Thr Asn Ala Thr Tyr 700 705 710			2164
cac tgc atc aag gat aac tgc ccc cat ctg cca aat tct ggg cag gaa His Cys Ile Lys Asp Asn Cys Pro His Leu Pro Asn Ser Gly Gln Glu 715 720 725			2212
gac ttt gac aag gac ggg att ggc gat gcc tgt gat gat gac gat gac Asp Phe Asp Lys Asp Gly Ile Gly Asp Ala Cys Asp Asp Asp Asp 730 735 740 745			2260
aat gac ggt gtg acc gat gag aag gac aac tgc cag ctc ctc ttc aat Asn Asp Gly Val Thr Asp Glu Lys Asp Asn Cys Gln Leu Leu Phe Asn 750 755 760			2308
ccc cgc cag gct gac tat gac aag gat gag gtt ggg gac cgc tgt gac Pro Arg Gln Ala Asp Tyr Asp Lys Asp Glu Val Gly Asp Arg Cys Asp 765 770 775			2356

aac tgc cct tac gtg cac aac cct gcc cag atc gac aca gac aac aat Asn Cys Pro Tyr Val His Asn Pro Ala Gln Ile Asp Thr Asp Asn Asn 780 785 790	2404
gga gag ggt gac gcc tgc tcc gtg gac att gat ggg gac gat gtc ttc Gly Glu Gly Asp Ala Cys Ser Val Asp Ile Asp Gly Asp Asp Val Phe 795 800 805	2452
aat gaa cga gac aat tgt ccc tac gtc tac aac act gac cag agg gac Asn Glu Arg Asp Asn Cys Pro Tyr Val Tyr Asn Thr Asp Gln Arg Asp 810 815 820 825	2500
acg gat ggt gac ggt gtg ggg gat cac tgt gac aac tgc ccc ctg gtg Thr Asp Gly Asp Gly Val Gly Asp His Cys Asp Asn Cys Pro Leu Val 830 835 840	2548
cac aac cct gac cag acc gac gtg gac aat gac ctt gtt ggg gac cag His Asn Pro Asp Gln Thr Asp Val Asp Asn Asp Leu Val Gly Asp Gln 845 850 855	2596
tgt gac aac aac gag gac ata gat gac gac ggc cac cag aac aac cag Cys Asp Asn Asn Glu Asp Ile Asp Asp Asp Gly His Gln Asn Asn Gln 860 865 870	2644
gac aac tgc ccc tac atc tcc aac gcc aac cag gct gac cat gac aga Asp Asn Cys Pro Tyr Ile Ser Asn Ala Asn Gln Ala Asp His Asp Arg 875 880 885	2692
gac ggc cag ggc gac gcc tgt gac cct gat gat gac aac gat ggc gtc Asp Gly Gln Gly Asp Ala Cys Asp Pro Asp Asp Asp Asn Asp Gly Val 890 895 900 905	2740
ccc gat gac agg gac aac tgc cgg ctt gtg ttc aac cca gac cag gag Pro Asp Asp Arg Asp Asn Cys Arg Leu Val Phe Asn Pro Asp Gln Glu 910 915 920	2788
gac ttg gac ggt gat gga cgg ggt gat att tgt aaa gat gat ttt gac Asp Leu Asp Gly Asp Gly Arg Gly Asp Ile Cys Lys Asp Asp Phe Asp 925 930 935	2836
aat gac aac atc cca gat att gat gat gtg tgt cct gaa aac aat gcc Asn Asp Asn Ile Pro Asp Ile Asp Asp Val Cys Pro Glu Asn Asn Ala 940 945 950	2884
atc agt gag aca gac ttc agg aac ttc cag atg gtc ccc ttg gat ccc Ile Ser Glu Thr Asp Phe Arg Asn Phe Gln Met Val Pro Leu Asp Pro 955 960 965	2932
aaa ggg acc acc caa att gat ccc aac tgg gtc att cgc cat caa ggc Lys Gly Thr Thr Gln Ile Asp Pro Asn Trp Val Ile Arg His Gln Gly 970 975 980 985	2980
aag gag ctg gtt cag aca gcc aac tcg gac ccc ggc atc gct gta ggt Lys Glu Leu Val Gln Thr Ala Asn Ser Asp Pro Gly Ile Ala Val Gly 990 995 1000	3028

ttt gac gag ttt ggg tct gtg gac ttc agt ggc aca ttc tac gta aac 3076
 Phe Asp Glu Phe Gly Ser Val Asp Phe Ser Gly Thr Phe Tyr Val Asn
 1005 1010 1015

 act gac cgg gac gac gac tat gcc ggc ttc gtc ttt ggt tac cag tca 3124
 Thr Asp Arg Asp Asp Asp Tyr Ala Gly Phe Val Phe Gly Tyr Gln Ser
 1020 1025 1030

 agc agc cgc ttc tat gtg gtg atg tgg aag cag gtg acg cag acc tac 3172
 Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln Val Thr Gln Thr Tyr
 1035 1040 1045

 tgg gag gac cag ccc acg cgg gcc tat ggc tac tcc ggc gtg tcc ctc 3220
 Trp Glu Asp Gln Pro Thr Arg Ala Tyr Gly Tyr Ser Gly Val Ser Leu
 1050 1055 1060 1065

 aag gtg gtg aac tcc acc acg ggg acg ggc gag cac ctg agg aac gcg 3268
 Lys Val Val Asn Ser Thr Thr Gly Thr Gly Glu His Leu Arg Asn Ala
 1070 1075 1080

 ctg tgg cac acg ggg aac acg ccg ggg cag gtg cga acc tta tgg cac 3316
 Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val Arg Thr Leu Trp His
 1085 1090 1095

 gac ccc agg aac att ggc tgg aag gac tac acg gcc tat agg tgg cac 3364
 Asp Pro Arg Asn Ile Gly Trp Lys Asp Tyr Thr Ala Tyr Arg Trp His
 1100 1105 1110

 ctg act cac agg ccc aag acc ggc tac atc aga gtc tta gtg cat gaa 3412
 Leu Thr His Arg Pro Lys Thr Gly Tyr Ile Arg Val Leu Val His Glu
 1115 1120 1125

 gga aaa cag gtc atg gca gac tca gga cct atc tat gac caa acc tac 3460
 Gly Lys Gln Val Met Ala Asp Ser Gly Pro Ile Tyr Asp Gln Thr Tyr
 1130 1135 1140 1145

 gct ggc ggg cgg ctg ggt cta ttt gtc ttc tct caa gaa atg gtc tat 3508
 Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser Gln Glu Met Val Tyr
 1150 1155 1160

 ttc tca gac ctc aag tac gaa tgc aga gat att taaacaagat ttgctgcatt 3561
 Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Ile
 1165 1170

 tccggcaatg ccctgtgcat gccatgggtcc ctaga 3596

<210> 2
 <211> 1172
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Val Trp Arg Leu Val Leu Leu Ala Leu Trp Val Trp Pro Ser Thr
 1 5 10 15
 Gln Ala Gly His Gln Asp Lys Asp Thr Thr Phe Asp Leu Phe Ser Ile
 20 25 30
 Ser Asn Ile Asn Arg Lys Thr Ile Gly Ala Lys Gln Phe Arg Gly Pro

		35					40					45				
Asp	Pro	Gly	Val	Pro	Ala	Tyr	Arg	Phe	Val	Arg	Phe	Asp	Tyr	Ile	Pro	
	50					55					60					
Pro	Val	Asn	Ala	Asp	Asp	Leu	Ser	Lys	Ile	Thr	Lys	Ile	Met	Arg	Gln	
65					70					75					80	
Lys	Glu	Gly	Phe	Phe	Leu	Thr	Ala	Gln	Leu	Lys	Gln	Asp	Gly	Lys	Ser	
				85					90					95		
Arg	Gly	Thr	Leu	Leu	Ala	Leu	Glu	Gly	Pro	Gly	Leu	Ser	Gln	Arg	Gln	
			100					105					110			
Phe	Glu	Ile	Val	Ser	Asn	Gly	Pro	Ala	Asp	Thr	Leu	Asp	Leu	Thr	Tyr	
		115					120					125				
Trp	Ile	Asp	Gly	Thr	Arg	His	Val	Val	Ser	Leu	Glu	Asp	Val	Gly	Leu	
	130					135					140					
Ala	Asp	Ser	Gln	Trp	Lys	Asn	Val	Thr	Val	Gln	Val	Ala	Gly	Glu	Thr	
145					150					155					160	
Tyr	Ser	Leu	His	Val	Gly	Cys	Asp	Leu	Ile	Asp	Ser	Phe	Ala	Leu	Asp	
				165					170					175		
Glu	Pro	Phe	Tyr	Glu	His	Leu	Gln	Ala	Glu	Lys	Ser	Arg	Met	Tyr	Val	
			180					185				190				
Ala	Lys	Gly	Ser	Ala	Arg	Glu	Ser	His	Phe	Arg	Gly	Leu	Leu	Gln	Asn	
		195					200					205				
Val	His	Leu	Val	Phe	Glu	Asn	Ser	Val	Glu	Asp	Ile	Leu	Ser	Lys	Lys	
	210					215					220					
Gly	Cys	Gln	Gln	Gly	Gln	Gly	Ala	Glu	Ile	Asn	Ala	Ile	Ser	Glu	Asn	
225					230					235					240	
Thr	Glu	Thr	Leu	Arg	Leu	Gly	Pro	His	Val	Thr	Thr	Glu	Tyr	Val	Gly	
				245					250					255		
Pro	Ser	Ser	Glu	Arg	Arg	Pro	Glu	Val	Cys	Glu	Arg	Ser	Cys	Glu	Glu	
			260					265					270			
Leu	Gly	Asn	Met	Val	Gln	Glu	Leu	Ser	Gly	Leu	His	Val	Leu	Val	Asn	
		275					280					285				
Gln	Pro	Ser	Glu	Asn	Leu	Lys	Arg	Val	Ser	Asn	Asp	Asn	Gln	Phe	Leu	
	290					295					300					
Trp	Glu	Leu	Ile	Gly	Gly	Pro	Pro	Lys	Thr	Arg	Asn	Met	Ser	Ala	Cys	
305					310					315					320	
Trp	Gln	Asp	Gly	Arg	Phe	Phe	Ala	Glu	Asn	Glu	Thr	Trp	Val	Val	Asp	
				325					330					335		
Ser	Cys	Thr	Thr	Cys	Thr	Cys	Lys	Lys	Phe	Lys	Thr	Ile	Cys	His	Gln	
			340					345				350				
Ile	Thr	Cys	Pro	Pro	Ala	Thr	Cys	Ala	Ser	Pro	Ser	Phe	Val	Glu	Gly	
		355					360					365				
Glu	Cys	Cys	Pro	Ser	Cys	Leu	His	Ser	Val	Asp	Gly	Glu	Glu	Gly	Trp	
		370				375					380					
Ser	Pro	Trp	Ala	Glu	Trp	Thr	Gln	Cys	Ser	Val	Thr	Cys	Gly	Ser	Gly	
385					390					395					400	

Trp	Ser	Pro	Trp	Ser	Pro	Trp	Ser	Ala	Cys	Thr	Val	Thr	Cys	Ala	Gly
			500					505					510		
Gly	Ile	Arg	Glu	Arg	Thr	Arg	Val	Cys	Asn	Ser	Pro	Glu	Pro	Gln	Tyr
		515					520					525			
Gly	Gly	Lys	Ala	Cys	Val	Gly	Asp	Val	Gln	Glu	Arg	Gln	Met	Cys	Asn
	530					535					540				
Lys	Arg	Ser	Cys	Pro	Val	Asp	Gly	Cys	Leu	Ser	Asn	Pro	Cys	Phe	Pro
545					550					555					560
Gly	Ala	Gln	Cys	Ser	Phe	Pro	Asp	Gly	Ser	Trp	Ser	Cys	Gly	Ser	
				565				570						575	
Cys	Pro	Val	Gly	Phe	Leu	Gly	Asn	Gly	Thr	His	Cys	Glu	Asp	Leu	Asp
			580					585					590		
Glu	Cys	Ala	Leu	Val	Pro	Asp	Ile	Cys	Phe	Ser	Thr	Ser	Lys	Val	Pro
		595					600					605			
Arg	Cys	Val	Asn	Thr	Gln	Pro	Gly	Phe	His	Cys	Leu	Pro	Cys	Pro	Pro
	610					615					620				
Arg	Tyr	Arg	Gly	Asn	Gln	Pro	Val	Gly	Val	Gly	Leu	Glu	Ala	Ala	Lys
625					630					635					640
Thr	Glu	Lys	Gln	Val	Cys	Glu	Pro	Glu	Asn	Pro	Cys	Lys	Asp	Lys	Thr
				645					650					655	
His	Asn	Cys	His	Lys	His	Ala	Glu	Cys	Ile	Tyr	Leu	Gly	His	Phe	Ser
		660						665					670		
Asp	Pro	Met	Tyr	Lys	Cys	Glu	Cys	Gln	Thr	Gly	Tyr	Ala	Gly	Asp	Gly
		675					680					685			
Leu	Ile	Cys	Gly	Glu	Asp	Ser	Asp	Leu	Asp	Gly	Trp	Pro	Asn	Leu	Asn
	690					695					700				
Leu	Val	Cys	Ala	Thr	Asn	Ala	Thr	Tyr	His	Cys	Ile	Lys	Asp	Asn	Cys
705					710					715					720
Pro	His	Leu	Pro	Asn	Ser	Gly	Gln	Glu	Asp	Phe	Asp	Lys	Asp	Gly	Ile
				725					730					735	
Gly	Asp	Ala	Cys	Asp	Asp	Asp	Asp	Asp	Asn	Asp	Gly	Val	Thr	Asp	Glu
		740					745					750			
Lys	Asp	Asn	Cys	Gln	Leu	Leu	Phe	Asn	Pro	Arg	Gln	Ala	Asp	Tyr	Asp
		755					760					765			
Lys	Asp	Glu	Val	Gly	Asp	Arg	Cys	Asp	Asn	Cys	Pro	Tyr	Val	His	Asn
	770					775					780				
Pro	Ala	Gln	Ile	Asp	Thr	Asp	Asn	Asn	Gly	Glu	Gly	Asp	Ala	Cys	Ser
785					790					795					800
Val	Asp	Ile	Asp	Gly	Asp	Asp	Val	Phe	Asn	Glu	Arg	Asp	Asn	Cys	Pro
			805						810					815	
Tyr	Val	Tyr	Asn	Thr	Asp	Gln	Arg	Asp	Thr	Asp	Gly	Asp	Gly	Val	Gly
		820						825					830		
Asp	His	Cys	Asp	Asn	Cys	Pro	Leu	Val	His	Asn	Pro	Asp	Gln	Thr	Asp
		835					840					845			
Val	Asp	Asn	Asp	Leu	Val	Gly	Asp	Gln	Cys	Asp	Asn	Asn	Glu	Asp	Ile
	850					855					860				
Asp	Asp	Asp	Gly	His	Gln	Asn	Asn	Gln	Asp	Asn	Cys	Pro	Tyr	Ile	Ser
865					870					875					880
Asn	Ala	Asn	Gln	Ala	Asp	His	Asp	Arg	Asp	Gly	Gln	Gly	Asp	Ala	Cys
			885					890						895	
Asp	Pro	Asp	Asp	Asp	Asn	Asp	Gly	Val	Pro	Asp	Asp	Arg	Asp	Asn	Cys
		900						905					910		
Arg	Leu	Val	Phe	Asn	Pro	Asp	Gln	Glu	Asp	Leu	Asp	Gly	Asp	Gly	Arg
		915					920					925			
Gly	Asp	Ile	Cys	Lys	Asp	Asp	Phe	Asp	Asn	Asp	Asn	Ile	Pro	Asp	Ile
	930					935					940				
Asp	Asp	Val	Cys	Pro	Glu	Asn	Asn	Ala	Ile	Ser	Glu	Thr	Asp	Phe	Arg

22

22

22

22

22

27

22

22

<400> 5
gaattctagg gaccatggca tgcac

25

<210> 6
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 6
Arg Glu Ser His Phe Arg Gly Leu Leu Gln Asn Val His Leu Val Phe
1 5 10 15

<210> 7
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 7
Pro Ala Thr Cys Ala Asn Pro Ser Phe Val Glu Gly Glu Cys Cys Pro
1 5 10 15
Ser Cys

<210> 8
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 8
Phe Ala Glu Asn Glu Thr Trp Val Val Asp Ser Cys Thr Thr Cys Thr
1 5 10 15
Cys Lys Lys Phe Lys Thr
20

<210> 9
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 9
Glu Leu Ile Gly Gly Pro Pro Lys Thr Arg Asn Met Ser Ala Cys
1 5 10 15

<210> 10

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetically generated peptide

<400> 10
Trp Ser Pro Trp Ala Glu Trp
1 5

<210> 11
<211> 6
<212> PRT
<213> Homo sapiens

<400> 11
Cys Ser Val Thr Val Gly
1 5